P. Mertz

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/684,383

DATE: 06/06/2002
TIME: 16:17:16

Input Set : N:\Crf3\RULE60\09684383.raw
Output Set: N:\CRF3\06062002\I684383.raw

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: H TTEN, Gertrud
NEIDHARDT, Helge
BECHTOLD, Rolf
POHL, Jens
PAULISTA, Michael

(ii) TITLE OF INVENTION: NEW GROWTH/DIFFERENTIATION FACTORS OF THE TGF- FAMILY

(iii) NUMBER OF SEQUENCES: 49

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: NIKAIDO, MARMELSTEIN, MURRAY & ORAM LLP
(B) STREET: 655 Fifteenth Street, N. W., G Street Lobby, Suite 330
(C) CITY: Washington
(D) STATE: DC
(E) COUNTRY: USA
(F) ZIP: 20005

ENTERED

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:
C--> **(A) APPLICATION NUMBER: US/09/684,383**
C--> **(B) FILING DATE: 10-Oct-2000**
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US/09/218,176
(B) FILING DATE:
(A) APPLICATION NUMBER: 08/679,048
(B) FILING DATE: 12-JUL-1996
(A) APPLICATION NUMBER: PCT/EP96/03065
(B) FILING DATE: 12-JUL-1996
(A) APPLICATION NUMBER: PCT/EP93/00350
(B) FILING DATE: 2-FEB-1993
(A) APPLICATION NUMBER: US 08/482,577
(B) FILING DATE: 7-JUN-1995
(A) APPLICATION NUMBER: EP 92 102 324.8
(B) FILING DATE: 12-FEB-1992
(A) APPLICATION NUMBER: DE P 44 23 190.3
(B) FILING DATE: 01-JUL-1994
(A) APPLICATION NUMBER: DE 195 11 243.1

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PATENT APPLICATION: US/09/684,383 TIME: 16:17:16

Input Set : N:\Crf3\RULE60\09684383.raw
Output Set: N:\CRF3\06062002\I684383.raw

(B) FILING DATE: 27-MAR-1995
(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: KITTS, Monica Chin
(B) REGISTRATION NUMBER: 36,105
(C) REFERENCE/DOCKET NUMBER: P564-6010
(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 202/638-5000
(B) TELEFAX: 202/638-4810
(2) INFORMATION FOR SEQ ID NO: 1:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2272 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
W--> **(ii) MOLECULE TYPE: DNA**
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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CAAGGAGCCA TGCCAGCTGG ACACACACTT CTTCCAGGGC CTCTGGCAGC CAGGACAGAG     60
TTGAGACCAC AGCTGTTGAG ACCCTGAGCC CTGAGTCTGT ATTGCTCAAG AAGGGCCTTC    120
CCCAGCAATG ACCTCCTCAT TGCTTCTGGC CTTTCTCCTC CTGGCTCCAA CCACAGTGGC    180
CACTCCCAGA GCTGGCGGTC AGTGTCCAGC ATGTGGGGGG CCCACCTTGG AACTGGAGAG    240
CCAGCGGGAG CTGCTTCTTG ATCTGGCCAA GAGAAGCATC TTGGACAAGC TGCACCTCAC    300
CCAGCGCCCA ACACTGAACC GCCCTGTGTC CAGAGCTGCT TTGAGGACTG CACTGCAGCA    360
CCTCCACGGG GTCCCACAGG GGGCACTTCT AGAGGACAAC AGGGAACAGG AATGTGAAAT    420
CATCAGCTTT GCTGAGACAG GCCTCTCCAC CATCAACCAG ACTCGTCTTG ATTTTCACTT    480
CTCCTCTGAT AGAACTGCTG GTGACAGGGA GGTCCAGCAG GCCAGTCTCA TGTTCTTTGT    540
GCAGCTCCCT TCCAATACCA CTTGGACCTT GAAAGTGAGA GTCCTTGTGC TGGGTCCACA    600
TAATACCAAC CTCACCTTGG CTACTCAGTA CCTGCTGGAG GTGGATGCCA GTGGCTGGCA    660
TCAACTCCCC CTAGGGCCTG AAGCTCAAGC TGCCTGCAGC CAGGGGCACC TGACCCTGGA    720
GCTGGTACTT GAAGGCCAGG TAGCCCAGAG CTCAGTCATC CTGGGTGGAG CTGCCCATAG    780
GCCTTTTGTG GCAGCCCGGG TGAGAGTTGG GGGCAAACAC CAGATTCACC GACGAGGCAT    840
CGACTGCCAA GGAGGGTCCA GGATGTGCTG TCGACAAGAG TTTTTTGTGG ACTTCCGTGA    900
GATTGGCTGG CACGACTGGA TCATCCAGCC TGAGGGCTAC GCCATGAACT TCTGCATAGG    960
GCAGTGCCCA CTACACATAG CAGGCATGCC TGGTATTGCT GCCTCCTTTC ACACTGCAGT   1020
GCTCAATCTT CTCAAGGCCA ACACAGCTGC AGGCACCACT GGAGGGGGCT CATGCTGTGT   1080
ACCCACGGCC CGGCGCCCCC TGTCTCTGCT CTATTATGAC AGGGACAGCA ACATTGTCAA   1140
GACTGACATA CCTGACATGG TAGTAGAGGC CTGTGGGTGC AGTTAGTCTA TGTGTGGTAT   1200
GGGCAGCCCA AGGTTGCATG GGAAAACACG CCCCTACAGA AGTGCACTTC CTTGAGAGGA   1260
GGGAATGACC TCATTCTCTG TCCAGAATGT GGACTCCCTC TTCCTGAGCA TCTTATGGAA   1320
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TGACCACTAC CCTCTTTCCT AGGGCATAGT CCATCCCGCT AGTCCATCCC GCTAGCCCCA   1440
CTCCAGGGAC TCAGACCCAT CTCCAACCAT GAGCAATGCC ATCTGGTTCC CAGGCAAAGA   1500
CACCCTTAGC TCACCTTTAA TAGACCCCAT AACCCACTAT GCCTTCCTGT CCTTTCTACT   1560
CAATGGTCCC CACTCCAAGA TGAGTTGACA CAACCCCTTC CCCCAATTTT TGTGGATCTC   1620
CAGAGAGGCC CTTCTTTGGA TTCACCAAAG TTTAGATCAC TGCTGCCCAA AATAGAGGCT   1680
TACCTACCCC CCTCTTTGTT GTGAGCCCCT GTCCTTCTTA GTTGTCCAGG TGAACTACTA   1740
AAGCTCTCTT TGCATACCTT CATCCATTTT TTGTCCTTCT CTGCCTTTCT CTATGCCCTT   1800
AAGGGGTGAC TTGCCTGAGC TCTATCACCT GAGCTCCCCT GCCCTCTGGC TTCCTGCTGA   1860
GGTCAGGGCA TTTCTTATCC CTGTTCCCTC TCTGTCTAGG TGTCATGGTT CTGTGTAACT   1920
GTGGCTATTC TGTGTCCCTA CACTACCTGG CTACCCCCTT CCATGGCCCC AGCTCTGCCT   1980
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Input Set : N:\Crf3\RULE60\09684383.raw
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ACATTCTGAT TTTTTTTTTT TTTTTTTTTT TGAAAAGTTA AAAATTCCTT AATTTTTTAT 2040
TCCTGGTACC ACTACCACAA TTTACAGGGC AATATACCTG ATGTAATGAA AAGAAAAAGA 2100
AAAAGACAAA GCTACAACAG ATAAAAGACC TCAGGAATGT ACATCTAATT GACACTACAT 2160
TGCATTAATC AATAGCTGCA CTTTTTGCAA ACTGTGGCTA TGACAGTCCT GAACAAGAAG 2220
GGTTTCCTGT TTAAGCTGCA GTAACTTTTC TGACTATGGA TCATCGTTCC TT 2272

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 352 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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Met Thr Ser Ser Leu Leu Leu Ala Phe Leu Leu Leu Ala Pro Thr Thr
1               5                  10                  15
Val Ala Thr Pro Arg Ala Gly Gly Gln Cys Pro Ala Cys Gly Gly Pro
            20                  25                  30
Thr Leu Glu Leu Glu Ser Gln Arg Glu Leu Leu Leu Asp Leu Ala Lys
        35                  40                  45
Arg Ser Ile Leu Asp Lys Leu His Leu Thr Gln Arg Pro Thr Leu Asn
    50                  55                  60
Arg Pro Val Ser Arg Ala Ala Leu Arg Thr Ala Leu Gln His Leu His
65                  70                  75                  80
Gly Val Pro Gln Gly Ala Leu Leu Glu Asp Asn Arg Glu Gln Glu Cys
                85                  90                  95
Glu Ile Ile Ser Phe Ala Glu Thr Gly Leu Ser Thr Ile Asn Gln Thr
            100                 105                 110
Arg Leu Asp Phe His Phe Ser Ser Asp Arg Thr Ala Gly Asp Arg Glu
        115                 120                 125
Val Gln Gln Ala Ser Leu Met Phe Phe Val Gln Leu Pro Ser Asn Thr
    130                 135                 140
Thr Trp Thr Leu Lys Val Arg Val Leu Val Leu Gly Pro His Asn Thr
145                 150                 155                 160
Asn Leu Thr Leu Ala Thr Gln Tyr Leu Leu Glu Val Asp Ala Ser Gly
                165                 170                 175
Trp His Gln Leu Pro Leu Gly Pro Glu Ala Gln Ala Ala Cys Ser Gln
            180                 185                 190
Gly His Leu Thr Leu Glu Leu Val Leu Glu Gly Gln Val Ala Gln Ser
        195                 200                 205
Ser Val Ile Leu Gly Gly Ala Ala His Arg Pro Phe Val Ala Ala Arg
    210                 215                 220
Val Arg Val Gly Gly Lys His Gln Ile His Arg Arg Gly Ile Asp Cys
225                 230                 235                 240
Gln Gly Gly Ser Arg Met Cys Cys Arg Gln Glu Phe Phe Val Asp Phe
                245                 250                 255
Arg Glu Ile Gly Trp His Asp Trp Ile Ile Gln Pro Glu Gly Tyr Ala
            260                 265                 270
Met Asn Phe Cys Ile Gly Gln Cys Pro Leu His Ile Ala Gly Met Pro
        275                 280                 285
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PATENT APPLICATION: US/09/684,383 TIME: 16:17:16

Input Set : N:\Crf3\RULE60\09684383.raw
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```
235  Gly Ile Ala Ala Ser Phe His Thr Ala Val Leu Asn Leu Leu Lys Ala
236      290                 295                 300
238  Asn Thr Ala Ala Gly Thr Thr Gly Gly Gly Ser Cys Cys Val Pro Thr
239  305                 310                 315                 320
241  Ala Arg Arg Pro Leu Ser Leu Leu Tyr Tyr Asp Arg Asp Ser Asn Ile
242                  325                 330                 335
244  Val Lys Thr Asp Ile Pro Asp Met Val Val Glu Ala Cys Gly Cys Ser
245              340                 345                 350
248 (2) INFORMATION FOR SEQ ID NO: 3:
250      (i) SEQUENCE CHARACTERISTICS:
251           (A) LENGTH: 1558 base pairs
252           (B) TYPE: nucleic acid
253           (C) STRANDEDNESS: single
254           (D) TOPOLOGY: linear
W--> 256     (ii) MOLECULE TYPE: DNA
259      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
261  AAGGAGTCAT GCCAGTCGGA GGTCAGTCAC ATTCCTCCCA GGGTCCCTGG TGCCCAGGAC    60
262  AGAGTTGAAG CACTCCCGTT GAGACCCTGA ATATAGGCTT TGGGTCCTTT AAGGAGGCTA   120
263  TCCTCCAGCA ATGGCCTCCT CCTTGCTCCT GGCTCTTCTG TTCCTGACTC CAACCACAGT   180
264  AGTGAACCCC AAAACTGAGG GTCCATGCCC AGCATGTTGG GGTGCCATCT TTGACCTGGA   240
265  GAGCCAGCGG GAGCTGCTTC TCGATTTGGC CAAGAAAAGT ATCCTGGACA AGCTGCACCT   300
266  CAGCCAGCGC CCCATACTCA GTCGGCCAGT GTCCAGAGGG GCTCTCAAGA CCGCGCTGCA   360
267  GCGCCTCCGC GGGCCTCGAC GGGAAACCCT GTTGGAGCAT GACCAGAGAC AAGAAGAATA   420
268  TGAGATCATC AGCTTTGCTG ACACAGACCT CTCCAGCATC AACCAGACCC GGCTCGAGTT   480
269  CCACTTCTCT GGTAGAATGG CCAGTGGCAT GGAGGTCCGG CAGACCCGCT TCATGTTCTT   540
270  CGTGCAGTTC CCCCACAATG CCACCCAGAC CATGAATATA AGAGTTCTTG TGCTAAGACC   600
271  ATATGACACC AACCTCACCT TGACAAGTCA GTACGTGGTG CAGGTGAATG CCAGTGGCTG   660
272  GTACCAGCTT CTCCTGGGAC CTGAAGCTCA AGCTGCTTGC AGCCAGGGAC ACCTTACTCT   720
273  GGAGCTGGTA CCAGAAAGCC AGGTGGCCCA CAGTTCCTTG ATCCTGGGCT GGTTTTCCCA   780
274  CAGGCCTTTT GTGGCAGCCC AGGTAAGGGT TGAGGGCAAG CATCGGGTTC GCCGGCGAGG   840
275  TATCGATTGC CAGGGGGGGT CCAGGATGTG CTGTCGACAA GAGTTTTTTG TAGACTTCCG   900
276  TGAGATTGGC TGGAATGACT GGATCATCCA GCCTGAAGGC TATGCCATGA ACTTCTGCAC   960
277  TGGGCAGTGC CCACTACATG TGGCAGGCAT GCCTGGCATC TCTGCCTCCT TTCACACTGC  1020
278  AGTGCTGAAT CTGCTCAAAG CCAACGCAGC TGCTGGCACC ACTGGCAGGG GCTCGTGCTG  1080
279  CGTGCCTACA TCTCGGCGCC CTCTGTCTTT GCTCTACTAT GACAGGGACA GCAACATTGT  1140
280  CAAGACGGAT ATACCTGACA TGGTGGTCGA GGCCTGCGGG TGTAGTTAGC TTATGGGTGA  1200
281  TACAGGCTGC CTGAGGTAGA ATGGCCTTCC TCAGGAAGGG AAACTCTGTT CCCACTTCTG  1260
282  TCCAGAATGG AAACACCTTT CTAAGCATGC AGACATCCCT CTGTGGACTT CAGGGGATCC  1320
283  ACCTCTAAAG AGAGTCACTA GTGACCAACA GCCTTTCTCT CTCCTGGGAC ATGGTTGACC  1380
284  CAGTACACCC ATCCTCAGCC TTAAGTTAGA GGCTAATCGA CTCCTACATA TATATGTCAT  1440
285  TTTGTCCTAG CAAACACCCC TTAGCTCCCC TTAGTCAACT ATGTAATCTA CTCTGCCTCC  1500
286  CTGACCCTGC CACCGGAAGG TTCCTATTCC ACGATGATAT GCCTTAGTGT CTCCCCTT    1558
288 (2) INFORMATION FOR SEQ ID NO: 4:
289      (i) SEQUENCE CHARACTERISTICS:
290           (A) LENGTH: 352 amino acids
291           (B) TYPE: amino acid
292           (C) STRANDEDNESS: single
293           (D) TOPOLOGY: linear
295      (ii) MOLECULE TYPE: peptide
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RAW SEQUENCE LISTING DATE: 06/06/2002
PATENT APPLICATION: US/09/684,383 TIME: 16:17:16

Input Set : N:\Crf3\RULE60\09684383.raw
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Ala Ser Ser Leu Leu Leu Ala Leu Leu Phe Leu Thr Pro Thr Thr
1 5 10 15
Val Val Asn Pro Lys Thr Glu Gly Pro Cys Pro Ala Cys Trp Gly Ala
20 25 30
Ile Phe Asp Leu Glu Ser Gln Arg Glu Leu Leu Leu Asp Leu Ala Lys
35 40 45
Lys Ser Ile Leu Asp Lys Leu His Leu Ser Gln Arg Pro Ile Leu Ser
50 55 60
Arg Pro Val Ser Arg Gly Ala Leu Lys Thr Ala Leu Gln Arg Leu Arg
65 70 75 80
Gly Pro Arg Arg Glu Thr Leu Leu Glu His Asp Gln Arg Gln Glu Glu
85 90 95
Tyr Glu Ile Ile Ser Phe Ala Asp Thr Asp Leu Ser Ser Ile Asn Gln
100 105 110
Thr Arg Leu Glu Phe His Phe Ser Gly Arg Met Ala Ser Gly Met Glu
115 120 125
Val Arg Gln Thr Arg Phe Met Phe Phe Val Gln Phe Pro His Asn Ala
130 135 140
Thr Gln Thr Met Asn Ile Arg Val Leu Val Leu Arg Pro Tyr Asp Thr
145 150 155 160
Asn Leu Thr Leu Thr Ser Gln Tyr Val Val Gln Val Asn Ala Ser Gly
165 170 175
Trp Tyr Gln Leu Leu Leu Gly Pro Glu Ala Gln Ala Ala Cys Ser Gln
180 185 190
Gly His Leu Thr Leu Glu Leu Val Pro Glu Ser Gln Val Ala His Ser
195 200 205
Ser Leu Ile Leu Gly Trp Phe Ser His Arg Pro Phe Val Ala Ala Gln
210 215 220
Val Arg Val Glu Gly Lys His Arg Val Arg Arg Arg Gly Ile Asp Cys
225 230 235 240
Gln Gly Gly Ser Arg Met Cys Cys Arg Gln Glu Phe Phe Val Asp Phe
245 250 255
Arg Glu Ile Gly Trp Asn Asp Trp Ile Ile Gln Pro Glu Gly Tyr Ala
260 265 270
Met Asn Phe Cys Thr Gly Gln Cys Pro Leu His Val Ala Gly Met Pro
275 280 285
Gly Ile Ser Ala Ser Phe His Thr Ala Val Leu Asn Leu Leu Lys Ala
290 295 300
Asn Ala Ala Ala Gly Thr Thr Gly Arg Gly Ser Cys Cys Val Pro Thr
305 310 315 320
Ser Arg Arg Pro Leu Ser Leu Leu Tyr Tyr Asp Arg Asp Ser Asn Ile
325 330 335
Val Lys Thr Asp Ile Pro Asp Met Val Val Glu Ala Cys Gly Cys Ser
340 345 350

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/684,383

DATE: 06/06/2002
TIME: 16:17:17

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Output Set: N:\CRF3\06062002\I684383.raw

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L:33 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
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